**Sequence results for 3rd colony with Forward Primer (FrTuHP in pNIC-Bsa4 cloning)**

>lcl|28597

Length=1056

Score = 1740 bits (942), Expect = 0.0

Identities = 968/991 (98%), Gaps = 2/991 (0%)

Strand=Plus/Plus

Query 89 ATGAAGAAAATCTTTGTTAGCTTTACTCTGCTCTTCTTCCTGATTCCGGTGGGTTACTCT 148

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1 ATGAAGAAAATCTTTGTTAGCTTTACTCTGCTCTTCTTCCTGATTCCGGTGGGTTACTCT 60

Query 149 TCTAAGCTGATCTTCGTGTCTATGATCACCCGTCACGGCGATCGTGCGCCGTTTGCGAAC 208

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 61 TCTAAGCTGATCTTCGTGTCTATGATCACCCGTCACGGCGATCGTGCGCCGTTTGCGAAC 120

Query 209 ATCGAAAACGCGAACTACTCTTGGGGTACCGAACTGTCTGAGCTGACCCCAATCGGTATG 268

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 121 ATCGAAAACGCGAACTACTCTTGGGGTACCGAACTGTCTGAGCTGACCCCAATCGGTATG 180

Query 269 AACCAGGAATACAATCTGGGTCTCCAGCTGCGTAAACGTTACATCGACAAATTCGGTCTG 328

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 181 AACCAGGAATACAATCTGGGTCTCCAGCTGCGTAAACGTTACATCGACAAATTCGGTCTG 240

Query 329 CTGCCGGAGCACTACGTTGACCAATCTATCTACGTCCTGTCTTCTCACACGAATCGTACC 388

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 241 CTGCCGGAGCACTACGTTGACCAATCTATCTACGTCCTGTCTTCTCACACGAATCGTACC 300

Query 389 GTTGTTTCTGCGCAATCTCTGCTGATGGGTCTGTACCCAGCGGGTACGGGTCCGCTGATC 448

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 301 GTTGTTTCTGCGCAATCTCTGCTGATGGGTCTGTACCCAGCGGGTACGGGTCCGCTGATC 360

Query 449 GGTGACGGCGACCCGGCAATCAAAGACCGTTTCCAGCCGATCCCGATCATGACCCTGTCT 508

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 361 GGTGACGGCGACCCGGCAATCAAAGACCGTTTCCAGCCGATCCCGATCATGACCCTGTCT 420

Query 509 GCGGACTCTCGTCTGATCCAGTTCCCGTACGAACAGTACCTGGCGGTTCTGAAAAAGTAC 568

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 421 GCGGACTCTCGTCTGATCCAGTTCCCGTACGAACAGTACCTGGCGGTTCTGAAAAAGTAC 480

Query 569 GTGTACAACAGCCCGGAGTGGCAAAACAAAACCAAAGAAGCGGCTCCGAACTTTGCCAAA 628

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 481 GTGTACAACAGCCCGGAGTGGCAAAACAAAACCAAAGAAGCGGCTCCGAACTTTGCCAAA 540

Query 629 TGGCAGCAAATCCTGGGTAATCGTATCTCTGGTCTGAACGACGTCATCACCGTTGGTGAC 688

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 541 TGGCAGCAAATCCTGGGTAATCGTATCTCTGGTCTGAACGACGTCATCACCGTTGGTGAC 600

Query 689 GTTCTGATCGTGGCCCAGGCGCATGGCAAGCCGCTGCCGAAAGGTCTGTCTCAAGAAGAC 748

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 601 GTTCTGATCGTGGCCCAGGCGCATGGCAAGCCGCTGCCGAAAGGTCTGTCTCAAGAAGAC 660

Query 749 GCGGACCAGATCATCGCGCTGACCGACTGGGGTCTGGCGCAGCAGTTCAAATCTCAGAAA 808

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 661 GCGGACCAGATCATCGCGCTGACCGACTGGGGTCTGGCGCAGCAGTTCAAATCTCAGAAA 720

Query 809 GTTTCTTACATCATGGGTGGTAAACTGACCAACCGTATGATCGAAGACCTCAACAACGCG 868

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 721 GTTTCTTACATCATGGGTGGTAAACTGACCAACCGTATGATCGAAGACCTCAACAACGCG 780

Query 869 GTTAATGGTAAATCTAAATACAAAATGACCTACTACTCCGGTCACGACCTCACCCTGCTC 928

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 781 GTTAATGGTAAATCTAAATACAAAATGACCTACTACTCCGGTCACGACCTCACCCTGCTC 840

Query 929 GAAGTTATGGGTACTCTGGGNGTTCCGCTGGACACCGCCCCAGGTTACGCGAGCAANNTG 988

|||||||||||||||||||| ||||||||||||||||||||||||||||||||||| ||

Sbjct 841 GAAGTTATGGGTACTCTGGGTGTTCCGCTGGACACCGCCCCAGGTTACGCGAGCAACCTG 900

Query 989 GNAATGGNACTGTACNNGN-TGGTGACNTCTACNNCNTNAAACTGCGTTANA-CGGCAAG 1046

| ||||| ||||||| | ||||||| ||||| | | ||||||||||| | |||||||

Sbjct 901 GAAATGGAACTGTACAAGGATGGTGACATCTACACCGTTAAACTGCGTTACAACGGCAAG 960

Query 1047 NNNGNNAAACTGCCTATCATGGNCNAAAACA 1077

| |||||||||||||||| | ||||||

Sbjct 961 TATGTGAAACTGCCTATCATGGACAAAAACA 991

**Sequencing Results for 3rd Colony with Reverse Primer (FrTuHP in pNIC-Bsa4 cloning)**

>lcl|12989

Length=1056

Score = 1784 bits (966), Expect = 0.0

Identities = 980/994 (99%), Gaps = 0/994 (0%)

Strand=Plus/Minus

Query 88 TTATTTCTGGAATTTTTCGTTGATAGACTGCATGTATTTGTTCAGAGCGTCCAGAGAGCA 147

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1056 TTATTTCTGGAATTTTTCGTTGATAGACTGCATGTATTTGTTCAGAGCGTCCAGAGAGCA 997

Query 148 AGAGTTGTTTTTGTCCATGATAGGCAGTTTCACATACTTGCCGTTGTAACGCAGTTTAAC 207

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 996 AGAGTTGTTTTTGTCCATGATAGGCAGTTTCACATACTTGCCGTTGTAACGCAGTTTAAC 937

Query 208 GGTGTAGATGTCACCATCCTTGTACAGTTCCATTTCCAGGTTGCTCGCGTAACCTGGGGC 267

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 936 GGTGTAGATGTCACCATCCTTGTACAGTTCCATTTCCAGGTTGCTCGCGTAACCTGGGGC 877

Query 268 GGTGTCCAGCGGAACACCCAGAGTACCCATAACTTCGAGCAGGGTGAGGTCGTGACCGGA 327

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 876 GGTGTCCAGCGGAACACCCAGAGTACCCATAACTTCGAGCAGGGTGAGGTCGTGACCGGA 817

Query 328 GTAGTAGGTCATTTTGTATTTAGATTTACCATTAACCGCGTTGTTGAGGTCTTCGATCAT 387

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 816 GTAGTAGGTCATTTTGTATTTAGATTTACCATTAACCGCGTTGTTGAGGTCTTCGATCAT 757

Query 388 ACGGTTGGTCAGTTTACCACCCATGATGTAAGAAACTTTCTGAGATTTGAACTGCTGCGC 447

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 756 ACGGTTGGTCAGTTTACCACCCATGATGTAAGAAACTTTCTGAGATTTGAACTGCTGCGC 697

Query 448 CAGACCCCAGTCGGTCAGCGCGATGATCTGGTCCGCGTCTTCTTGAGACAGACCTTTCGG 507

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 696 CAGACCCCAGTCGGTCAGCGCGATGATCTGGTCCGCGTCTTCTTGAGACAGACCTTTCGG 637

Query 508 CAGCGGCTTGCCATGCGCCTGGGCCACGATCAGAACGTCACCAACGGTGATGACGTCGTT 567

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 636 CAGCGGCTTGCCATGCGCCTGGGCCACGATCAGAACGTCACCAACGGTGATGACGTCGTT 577

Query 568 CAGACCAGAGATACGATTACCCAGGATTTGCTGCCATTTGGCAAAGTTCGGAGCCGCTTC 627

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 576 CAGACCAGAGATACGATTACCCAGGATTTGCTGCCATTTGGCAAAGTTCGGAGCCGCTTC 517

Query 628 TTTGGTTTTGTTTTGCCACTCCGGGCTGTTGTACACGTACTTTTTCAGAACCGCCAGGTA 687

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 516 TTTGGTTTTGTTTTGCCACTCCGGGCTGTTGTACACGTACTTTTTCAGAACCGCCAGGTA 457

Query 688 CTGTTCGTACGGGAACTGGATCAGACGAGAGTCCGCAGACAGGGTCATGATCGGGATCGG 747

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 456 CTGTTCGTACGGGAACTGGATCAGACGAGAGTCCGCAGACAGGGTCATGATCGGGATCGG 397

Query 748 CTGGAAACGGTCTTTGATTGCCGGGTCGCCGTCACCGATCAGCGGACCCGTACCCGCTGG 807

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 396 CTGGAAACGGTCTTTGATTGCCGGGTCGCCGTCACCGATCAGCGGACCCGTACCCGCTGG 337

Query 808 GTACAGACCCATCAGCAGAGATTGCGCAGAAACAACGGTACGATTCGTGTGAGAAGACAG 867

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 336 GTACAGACCCATCAGCAGAGATTGCGCAGAAACAACGGTACGATTCGTGTGAGAAGACAG 277

Query 868 GACGTAGATAGATTGGTCAACGTAGTGCTCCGGCAGCAGACCGAATTTGTCGATGTAACG 927

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 276 GACGTAGATAGATTGGTCAACGTAGTGCTCCGGCAGCAGACCGAATTTGTCGATGTAACG 217

Query 928 TTTACGCAGCTGGAGACCCAGATTGTATTCCTGGTTCATACCGATTGGGGTCAGCTCAGA 987

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 216 TTTACGCAGCTGGAGACCCAGATTGTATTCCTGGTTCATACCGATTGGGGTCAGCTCAGA 157

Query 988 CANTTCGGTACCCCAAGAGTAGTTCGNGTTTTCNATGNTCGCAAACGGCGCACGATCGNC 1047

|| ||||||||||||||||||||||| |||||| ||| |||||||||||||||||||| |

Sbjct 156 CAGTTCGGTACCCCAAGAGTAGTTCGCGTTTTCGATGTTCGCAAACGGCGCACGATCGCC 97

Query 1048 NNGANGGGNGATCATAGNCNCNANNATCAGCTTA 1081

|| ||| |||||||| | | | |||||||||

Sbjct 96 GTGACGGGTGATCATAGACACGAAGATCAGCTTA 63